

```

DM of: US-09-652-292-2 to: EST: * out_format : pfs
Date: Mar 15, 2002

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL:frame=_pnn,model -DEV=x1h
-Q-/cnr12-1/usptospool/US06522292/runat_11032002_161725_3195/app_q
-DB=EST -QMT=fastap -SUFFIX=rst -GAPOP=12,000 -GAPEXT=4,000
-MINMATCH=0.100 -LOOP1=0.000 -LOOP2=0.000 -XGAP=4,500
-QGAPEXT=0.050 -XGAPOP=10,000 -XGAPEXT=0.500 -TGAPOP=6,000
-FGAPEXT=7,000 -YGAPOP=10,000 -YGAPEXT=0.500 -DELOP=6,000
-DELIST=7,000 -START=1 -MATRIX=blossom -TRANS=human0.cdi
-DELIST=45 -DOCALIN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0
-ALIGN=15 -MODE=LOCAL -OUTPMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09652292 -EGCN1_1-4076
-NCPU=6 -CPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPPY -WAIT -THREADS=1

Search information block:
Query: US-09-652-292-2

Database sequences: 11351937
Database length: 1077921985
Database time length: 1204 940000

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APEN=4.000
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POP=6.000
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man1.0,cd1
N1.1=4076
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TIMEOUT=30
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seq_name: qb_gss:CN506MME
LOCUS      270.50 339.85 9.1e-10 1054 1 AL405660 T3 end of clone AU
DEFINITION AL449917 AL449917 Homo sapie
prime, mRNA sequence.
ACCESSION AL554162
VERSION AL554162.1 GI:12894675
SOURCE      EST.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eulacostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
KEYWORDS   human.
REFERENCE  1 (bases 1 to 910)
AUTHORS   Li.-W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    unpublished (2001)
COMMENT    Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr

```

score_list:	Strd	Orig	ZScore	EScore	Len	Documentation
Sequence_list:						
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ggb.est1:AL449914	-	786..00	1007..12	6.2e-10	466	AL449914 Homo sapiens
ggb.est1:AL449887	+	781..00	1000..87	1.4e-46	459	AL449887 Homo sapiens
ggb.est1:AL449913	+	770..00	986..75	8.3e-16	461	AL449913 Homo sapiens
ggb.est1:AL449886	+	742..00	951..14	8.2e-44	450	AL449886 Homo sapiens
ggb.est1:AL449886	+	689..00	881..62	6.1e-40	540	BE237601_146953 MARC 4BOV Bos
ggb.est1:BE231601	+	623..00	791..00	6.8e-35	1049	BF681799_6021849821 NIH_MGC_1
ggb.est2:BF688799	+	553..00	708..65	2.6e-30	481	BF706971_281657 3BOV Bos_1
ggb.est2:BF706979	+	473..00	610..46	7.7e-25	306	AA313045 EST183920 Pancreas tun
ggb.est1:AA313045	+	445..00	572..10	1.1e-22	402	AA449905 Homo sapiens
ggb.est2:BF615211	+	433..00	555..93	9.3e-22	513	BF615211_0882204 x1 Wellcome Cl
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ggb.est1:AA164852	+	377..00	489..56	4.2e-18	248	AA164852 vE55g08 y1 Soares_mamm
ggb.est2:BF611497	+	356..00	455..74	3.1e-15	691	BF611497_0882404 y1 Wellcome Cl
ggb.gss:INS0.9BV	+	353..00	446..24	3.1e-15	966	Tetraedron nigroviridis
ggb.est2:BF785282	+	332..00	421..74	2.5e-14	747	FE789282_602105191F1 NC1_CGAP_1
ggb.est1:AA15084	+	332..00	412..60	8.1e-14	2003	AA118767_090018 RCW Lambda Zaf
ggb.est1:AL118747	+	320..50	408..73	1.3e-13	622	AL118767_BPF7P61020_1r1 761
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ggb.est1:BE61687	+	294..00	384..66	2.9e-12	215	AA494668 Homo sapiens
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ggb.est1:AL449471	-	291..00	381..00	4.7e-12	211	AA449916 Homo sapiens
ggb.est1:AL449916	+	291..00	368..93	2.2e-11	775	BE662822_C12_5_B13_SS6 Cerat
ggb.est1:BE61682	+	289..00	378..75	6.2e-11	204	AA461907_v195908_r1 Soares_mamm
ggb.est2:BF328407	+	288..50	377..98	6.9e-12	207	BF328B07 PMI-BN0174-210500-006
ggb.est2:BF328407	+	285..00	364..45	3.9e-11	549	AW97533_10995 MARC 1BOV Bos
ggb.est1:AL657233	+	284..00	373..51	2.2e-10	180	AL449826_0478h01_1y1 Wellcome Cl
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ggb.est1:AW561030	+	280..00	355..85	1.2e-10	746	AV381822_0478h01_1y1 Wellcome Cl
ggb.est1:AV381822	+	279..50	353..60	1.6e-10	824	BF033803_601454148F1 NIH_MGC_6
ggb.est2:BF328403	+	275..50	349..88	2.5e-10	712	BFS34681 EST353573 tomato flower
ggb.est1:AW934681	+	275..00	347..55	3.4e-10	855	AW980827 GM_UMB001_151_716F UMF
ggb.est1:AW910827	+	274..50	351..05	2.2e-10	548	AW9826 GM_UMB001_151_716F UMF
ggb.gss:0989426	+	273..00	343..53	7.1e-10	1000	AL175247 T7 end of clone AX0A
ggb.est2:R590842	+	273..00	349..27	5.1e-10	522	5590842_17112001_1y1 Wellcome Cl



VERSION AL449887.1 GI:11181512

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 459)

AUTHORS Stavrides, G.S., Huckle, E.J. and Deloukas, P.

TITLE Unpublished. Stavrides, G.S., Huckle, E.J. and Deloukas, P.

JOURNAL (2000)

COMMENT Contact: Stavrides GS

The Sanger Centre

Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK

Email: humquery@sanger.ac.uk

Sanger Centre name : sccd138.

FEATURES source

1. 459 /organism="Homo sapiens" /db\_xref="taxon:9606" /map="20" /clone\_lib="Homo sapiens fetal lung (Stavrides GS)" /tissue\_type="Lung" /dev\_stage="fetal" /note="cDNA fragment isolated using a cDNA end rescue technique"

BASE COUNT 74 a 142 g 95 t

ORIGIN

alignment\_scores:

Quality: 781.00	Length: 153
Ratio: 5.105	Gaps: 0
Percent Similarity: 100.000	Percent Identity: 99.346

alignment\_block: US-09-652-292-2 x AL449887 ..

Align seg 1/1 to: AL449887 from: 1 to: 459

162 Trp Gly Trp Arg His Met Phe Arg Ile Phe Leu Alanine G1 178

1 TGGGGATGGGGCACATGTCGGCTGGCCACTGACCTGCTCTGGCA 50

178 nsTerLeuSerLeuPheLeuProAlaGlyThrAspGluThrAlaThrH 195

51 ATCCCCTAGCCCTCCCTCCCTCCCTGGCCACGCCATACAC 100

195 Lys Lys Ser Leu Ile Pro Leu Glu Gly Glu Alanine Gln 200

101 AAAGGACCCATCCCACTCCAGGGGGTGAAGCCGCCAACCTGCCCG 150

212 Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Ile Arg Alanine G1 228

151 GGAGGCCACGGTACACTCCCTCTGGCCCTCAGGGCACGCCATACAT 200

228 Lys Arg Arg Thr Thr Val Gly Leu Gly Leu Alanine Gln 245

201 GCGAGCCGACACAAGCTGGCTGTGCTCTCCAGCAACTAA 250

245 Arg Gly Ser Asn Val Leu Leu Alanine Gln 261

251 CAGGGCAGCCAAACGCTGCTATGCCCTCACCATCTTCAGCTCGTT 300

262 Gly Phe His Gly Gly Ser Ser Alanine Leu Alanine Gln 278

301 GCTTCATGGGAACTCTCAGGGGAGCTGCGCTCTGGCCCTGGCC 350

278 Val Alanine Val Leu Alanine Ser Alanine Gln 295

351 AGTGAAGGTGGCAAGTACCCCTGACCCATGGGCTGGTGCAG 400

295 Lys Arg Alanine Leu Alanine Gly Alanine Leu Alanine Ser Val 311

113 erLeuSerSerNetAlaCysSilyleryValSerGluLeuValGlyPro 129

401 GCCGCAAGGGCTCTGCTAGCTGGCTGTCATGGCCCTGTCGTC 450

312 SerGlyIle 314

451 AGTGGCATA 459

seq\_name: qb\_est1:AL449913

seq\_documentation\_block:

LOCUS AL449913 mRNA

DEFINITION Homo sapiens fetal lung (Stavrides GS)

VERSION AL449913

ACCESSION AL449913.1 GI:11181538

EST.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 461)

AUTHORS Stavrides, G.S., Huckle, E.J. and Deloukas, P.

TITLE Unpublished (2000)

JOURNAL Unpublished (2000)

COMMENT Contact: Stavrides GS

The Sanger Centre

Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK

Email: humquery@sanger.ac.uk

Sanger Centre name : sccd334.

FEATURES source

1. 461 /organism="Homo sapiens" /db\_xref="taxon:9606" /map="20" /clone\_lib="Homo sapiens fetal lung (Stavrides GS)" /tissue\_type="Lung" /dev\_stage="fetal" /note="cDNA fragment isolated using a cDNA end rescue technique"

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ORIGIN

alignment\_scores:

Quality: 770.00	Length: 153
Ratio: 5.033	Gaps: 0
Percent Similarity: 100.000	Percent Identity: 100.000

alignment\_block: US-09-652-292-2 x AL449913 ..

Align seg 1/1 to: AL449913 from: 1 to: 461

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2 TCAGGTCGCCCTGGCTGCACATGCGTGACTTGGCTAACCTGCTGGA 51

46 uGlnGluPheLeuValGlySerLeuLeuLeuGlyAlanineAlaSerL 63

52 GCAGGACTCTCTGGTGGCAGCTGCCTGCCTGCCTGCCTCC 101

63 euValGlyGlyPheLeuIleAspCysteIleArgLysGlnAlanineLeu 79

102 TGGTTGGCTGGCTCCMCATGACTGCTATGGCAGGAAGCAGCCATCC 151

80 GlySerAsnLeuValLeuLeuAlanineGlySerLeuThrLeuGlyLeuAlaG1 96

152 GGGAGCACTGGCTGCGTGCAGCTGCGCC 201

96 ySerLeuAlaThrLeuValLeuGlySerLeuAlanineGlyPheAlaIleS 113

202 TICCCCTGGCCCTGGCTGCTCCGGCCGCGCTGGCTGCGCTGCGATTT 251

seq\_name: 9b\_est1:AL449886

seq\_documentation\_block:

LOCUS AL449886 450 bp mRNA EST 15-NOV-2000

DEFINITION Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA, mRNA sequence.

ACCESSION AL449886.1 GI:11181511

KEYWORDS EST.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Bos..

FEATURES

REFERENCE 1 (bases 1 to 450)

AUTHORS Stavrides, G.S., Huckle, E.J. and Deloukas, P.

TITLE Unpublished.

JOURNAL Unpublished (2000)

COMMENT Contact: Stavrides GS

The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, UK

Email: [hunquery@sanger.ac.uk](mailto:hunquery@sanger.ac.uk)

Sanger Centre name : scc01336.

Location/Qualifiers 1..450

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/map="20"

/clone\_id="Homo sapiens fetal lung (Stavrides GS)"

/tissue\_type="lung"

/dev\_stage="fetal"

/note="cDNA fragment isolated using a cDNA end rescue technique"

BASE COUNT 75 a 148 C 133 g 94 t

ORIGIN

align\_scores:

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Percent Similarity:	98.621	Percent Identity:	98.621

align\_block:

US-09-652-292-2 x AL449886 ..

Align seq 1/1 to: AL449886 from: 1 to: 450

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116 GGAATTCGGCACCGGGAGATCGCTGGTCCCTCTAGGGCAGGATCAC 65

144 rValGlyIleLeuLeuSerTyralaLeuAsnTyralaLeuAlaGlyThrP 161

66 CTTGGGCAATCCCTGCTTCCTATGCCCTCAACTATGCACCTGCTGTACCC 115

/note="vector: pcMV SPORT6; Site\_1: xbaI; Site\_2: xhoI;

7 -.

161 roTrPGlyTrpArgHsMetPheGlyTrpAlaThrAlaProAlaValLeu 177

116 CCTGGGGAGGGAGCAAGTTCTGGCTGGCACATGCACCTGGTCCCTG 165

178 GlnSerLeuSerLeuLeuProAlaGlyIlethAspGluThrAlaL 194

166 CAATCCCTAGCCCTCTTCCTGCTGAGATGAGACTGCAC 215

194 ThrLysAspLeuIleProLeuGlyLysGluAlaProLeuGlyIle 211

216 ACACAAAGGACCTGATCCACACTCAGGGAGGTAGGCCCAAGCTGCC 265

211 roGlyArgProArgGlySerPheLeuAspLeuPheArgAlaArgAsn 227

266 CGGGAGGGACCGCTACCTCTGGACCTCTGGCACCCGATGAAAC 315

228 MetArgGlyArgThrThrValGlyLeuGlyLeuValLeuPheGlnGlnLe 244

316 ATGGGAGGGACCACTGGCCCTGGGCTGGCTCTCCAGCAACT 365

244 uThrGlyGlnProAsnValLeucGlyIleSerThrIlePheSerIle 261

366 AACAGGGAGCCCAACCTGCTGGCTAGGCCCTCACCATCTCAGCTCCG 415

261 alGlyPheHisGlyLysSerSerAlaValLeuAla 272

416 TGGTTTCATGGGGATCCTAGGCCGTGCTGGCC 450

seq\_name: 9b\_cst1:BE237601

seq\_documentation\_block:

LOCUS BE237601 540 bp mRNA EST 25-APR-2001

DEFINITION 146553 MARC 4E0V Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE237601.1 GI:9022319

KEYWORDS EST.

SOURCE

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Bos..

REFERENCE 1 (bases 1 to 540)

AUTHORS Smith, T.P.L., Gross, W.M., Prekking, B.A., Roberts, A.J., Stone, R.T., Cass, E., Wray, J.E., Cho, J., Fairhurst, S.C., Bennett, G.L., Walton, M.P., Leegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: [smith@mail.marc.usda.gov](mailto:smith@mail.marc.usda.gov)

Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and mismatch 12 options.

PCR PRIMERS

FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCAGGACG

Plate: 48 row: P column: 4

Seq primer: ATTAGGTGACATATAG.

Location/Qualifiers 1..540

/organism="Bos taurus"

/db\_xref="taxon:9913"

/clone\_id="MARC 4E0V"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="vector: pcMV SPORT6; Site\_1: xbaI; Site\_2: xhoI;"

COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov Tissue Procurement: ANCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Icyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
FEATURES source	<p>Plate: LLCM156 row: d column: 22</p> <p>High quality sequence stop: 635.</p> <p>Location/Qualifiers</p> <p>1. .1049 /organism="Homo sapiens" /db_xref="taxon:3606" /clone="IMAGE:4294237" /clone.lib="NIH MGC-43" /issue_type="normal pigmented retinal epithelium" /lab_host="DH10B (phage-resistant)." /note="Organ: eye; Vector: pOTB1; Site_2: EcoRI; cDNA made by oligo-dT priming, Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCGAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library.  "</p>		
BASE COUNT ORIGIN	231 a 331 c 229 g 258 t		
alignment_scores:			
Quality:	623.00	Length:	122
Ratio:	5.107	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	99.180
alignment_block:	US-09-652-292-2 x BF688799 ..		
Align seg 1/1 to: BF688799 from: 1 to: 1049			
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5 GTCACTGGCCATCTCCTTGCGTTAGGCCAGTGACCTGGCTTCAGTCAG 54			
436 rGluLlePproValGluLleArgLleArgAlaHeAlaPheCysBnS 453			
55 CGAGATCTACCTGGAGATGGAGAGCTTCGCTTCAGCTCAACA 104			
453 erPheAsnTrpAlaAlaAsnLeuPheIleSerLeuSerPheLeuAspLeu 469			
105 GCTTCAACTGGGGCAACCTCTCATAGCCCTTCCTCTCATCTC 154			
470 IleGlyThrIleGlyLeuSerTrpThrPheLeuLeuTyroLeuThrI 486			
155 ATTGGCACCATGGCTTGCGCTTCGACGCTACGGCTACGGCTACCGC 204			
486 aValLeuGlyLeuGlyPheIleIleLeuPheValIProGluThrLysGly 503			
205 TGTGCTCGGCCGCTGGCTTCACTTTATTGGTCCTGAGACAAAGGCC 254			
503 IsoleuAlaGluIleAspGlnGlnPheGlnLysArgArgPheThrLeu 519			
255 AGTCGTTGGCAGAGATAACCAAGCTCCACTGGATCCAGAACGACGGTCACCCCTG 304			
520 ProGlyLysArgGlnAsnSerIleGlyIlePheTyrosArgIleG 536			
305 AGCTTGGCACAGGCAAGACTCCACTGGATCCAGAACGACGGTCACCCCTG 354			
536 uIleSerAlaAlaSer 541			
355 GATCCTGGGCCCTCC 370			

seq_name: gb_est1.BF706976	seq_documentation_block:	EST	25-APR-2001
LOCUS	BF706976	481 bp	mRNA
DEFINITION	281657 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.		
ACCESSION	BF706976		
VERSION	BF706976.1	GI:11998637	
KEYWORDS	EST.		
SOURCE			
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthidae; Bos.		
AUTHORS	Bovidae; Bovinae; Bos.		
1 (bases 1 to 481)	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casses, E., Wray, J.E., White, J., Cho, J.-J., Fahrerkrug, S.C., Bennett, G., Heaton, M.P., Laerdeid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Periea, G., Holt, I., Karaymycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.		
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle		
JOURNAL	Genome Res. 11 (4), 626-630 (2001)		
MEDLINE			
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov		
PCR PRIMERS	Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.		
FORWARD	AGGAACAGCTATGACCAT		
BACKWARD	GTTTCCAGTCAGCAG		
PLATE	79	row: F column: 16	
PLATE	79	row: F column: 16	
Seq primer: ATTAGGTGCACTATAG.			
FEATURES	Location/Qualifiers		
source	1..481		
/organism="Bos taurus"			
/db_xref="taxon:9913"			
/clone_id="MARC 3BOV"			
/tissue_type="pooled"			
/lab_host="DRI0B"			
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XbaI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."			
BASE COUNT	53 a 169 c 158 g 101 t		
ORIGIN			
alignment_scores:	Quality: 553.00	Length: 132	
	Ratio: 4.42	Gaps: 0	
	Percent Similarity: 94.697	Percent Identity: 87.121	
align seg 1/1 to: BF706976	from: 1 to: 481		
1 MetGlyHisSerProProValLeuproLeucyslaservalserLeute	17		
86 AtGGCCGACCTTCACTCTCCGCTCTAGAGGCCCTCGTGTCTGCT	135		
17 uGlyGlyLeuThrAspGlyLeusSerCysLeuGluGlnGluPhleu	34		
136 GGTTGGCTGACCTTGCATGACGTCATGCGGCCCTG	185		
34 euProteinClnLeuAspGlyLeusSerCysLeuGluGlnGluPhleu	50		
186 TGGCGCTGAGCTGATTCGGCTGATTCGGAGCTGCTG	235		
seq_name: gb_est1.BF706976	seq_documentation_block:	EST	19-APR-1997
LOCUS	BF706976	306 bp	mRNA
DEFINITION	Homo sapiens cDNA 5' end similar to sim1 to glucose transporter, mRNA sequence.		
ACCESSION	AA313045		
VERSION	AA313045.1	GI:1965446	
KEYWORDS	EST.		
ORGANISM	Homo sapiens		
REFERENCE	AA313045	306 bp	mRNA
AUTHORS	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulmer, R.A., Bult, C.J., Lee, N.H., Kirchner, E.F., Weinstock, K.G., Gocayne, J.D., Clayton, R.A., Sutton, G., Blake, J.A., Brandon, R.C., Man, W.A., C., Cline, T.R., Corlton, M.D., Earle, Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Gledhill, C.L., Gneim, C.L., Hanna, M.C., Hedblom, E., Hinke, P.S.J.R., Kelley, J.M., Moreno-Palangues, R.F., McDonald, L.A., Merrick, J.M., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Nguyen, D.T., Saudek, D.M., Shirley, R., Small, K.W., Spriggs, T.R., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Li, H., Meissner, P.S., Olsen, H., Raymond, P.J., Wei, Y.F., Wing, J., Xu, C., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haselein, W.A., Fields, C., Fraser, C.M., and Venter, J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence		
JOURNAL	Nature 377 (6547 Suppl.), 3-174 (1995)		
MEDLINE	96026280		
COMMENT	Contact: Kerlavage, AR		
Bioinformatics	The Institute for Genomic Research		
FEATURES	9712 Medical Center Drive, Rockville, MD 20850 USA		
source	tel: 3018699056		
	Fax: 3018699423		
	Email: akerlav@tigr.org		
	For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/db/ngi/hgi.html">http://www.tigr.org/db/ngi/hgi.html</a> )		
	seq primer: M13 Reverse.		
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1 MetGlyHisSerProProValLeuproLeucyslaservalserLeute	17		
86 AtGGCCGACCTTCACTCTCCGCTCTAGAGGCCCTCGTGTCTGCT	135		
17 uGlyGlyLeuThrAspGlyLeusSerCysLeuGluGlnGluPhleu	34		
136 GGTTGGCTGACCTTGCATGACGTCATGCGGCCCTG	185		
34 euProteinClnLeuAspGlyLeusSerCysLeuGluGlnGluPhleu	50		
186 TGGCGCTGAGCTGATTCGGCTGATTCGGAGCTGCTG	235		



Possible reversed clone; similarity on wrong strand  
 Seq. Primer: -40UP from Gibco  
 High quality sequence stop: 444.

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 /note="Vector: pCDNA1; Site\_1: NotI; Site\_2: EcoRI; cDNAs  
 were oligo-dT primed and directionally cloned. Library was  
 constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.  
 Gurdon (Wellcome/CRC Institute)."  
 BASE COUNT 138 a 113 c . 122 g 140 t  
 ORIGIN US-09-652-292-2 x BF615211 ..

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 Percent Similarity: 71.598 Percent Identity: 52.071

alignment\_block:  
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421 rAlaPheSerPheGlyPheGlyProValThrTrpLeuValSerGluI 438  
 58 TGCCTTTCTCATGGATTGTTGCTCAATGACCTGCTGTTAGTCAGTGAAA 107

438 leuTrpProValGluIleArgGlyArgAlaPheAlaPheCysAsnSerhe 454  
 108 TCTATCCAGGGACATCAGGGAGAGATTTCTGTCGACAGCTC 157

455 AsnTrpAlaAlaLysLeuPheIleSerLeuLeuAspLeuIleG1 471  
 158 AACGGGGCTGCCAACCTGCTCATACCTTACCTTACCTTATGGTATGG 207

471 ythrIleGlyLeuSerTrpThrPheLeuLeuThrGlyLeuThrAlaValI 488  
 208 TTCTATAGGTCTGGCTGACTCTTGTGCTGACGGGGGGGGCGCTGC 257

488 euGlyLeuGlyPheIleIleArgValPheValProGluThrLysGlyGlnSer 504  
 258 TGGCCATATGCCATTCATCATCATCATCATCATCATCATCATCATCAT 307

505 LeuAlaGluIleAspGlnPhe.Gln..... 513

308 CTCGAAGAAATCCATCAACAGTTACAGATTCAGGATATCAAGAGAGAGA 357

513 ..... 513

358 TAACCAGGAAAGTGAGTGCGCATGGAGAAAGGTTCGCCAGGGCTCAG 407

514 ..... 514

408 GAAAACAGCACATGCCAATAACATGTTATCAAGGATATCAAGAGAGAGA 457

517 ehrleUserPheGlyHisArgGlnAsnSerThrGlyIleProtrySerA 534  
 458 AACATCTAAAGGCCGTCGAAAGAACCATCCACTGCCCTACATACCAAA 507

534 ArgIle 535  
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seq\_name: qb\_est2:BF612918  
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 LOCUS BF612918 491 bp mRNA EST 14-DEC-2000  
 DEFINITION dd78h01.x2 Wellcome CRC pCDNA1 egg Xenopus laevis cDNA clone  
 IMAGE:3430512 3, similar to TR:095528 O95528 DH28H20.1 ; mRNA  
 sequence.  
 ACCESSION BF612918  
 VERSION BF612918.1 GI:11784031  
 KEYWORDS EST  
 SOURCE African clawed frog.  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Ppoidae; Ppidae;  
 Xenopodinae; Xenopus.  
 REFERENCE 1 (bases 1 to 491)  
 AUTHORS Clifton, S., Johnson, S.L., Blumberg, B., Song, J.J., Hillier, L., Pape, D., Martin, J., Wyllie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R., and Wilson, R.  
 Other ESTs: dG78h01.y1  
 Unpublished (1999)  
 Contact: Sandy Clifton, Ph.D.  
 WashU Xenopus EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@washu.edu  
 Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon, (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: Xenopus Clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov  
 Possible reversed clone; similarity on wrong strand  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 452.  
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 BASE COUNT 131 a 107 c 116 g 136 t 1 others  
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 Ratio: 3.938 Gaps: 0  
 Percent Similarity: 94.595 Percent Identity: 69.369  
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Align seg 1/1 to: BF612918 from: 1 to: 491

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 8 TATGCCATTGAACTGGATAACCTGCTCATACCTTACCTTATGGTATGG 207

421 rAlaPheSerPheGlyPheGlyProValThrTrpLeuValSerGluI 438  
 58 TGCCTTTCTCATGGATTGTTGCTCAATGACCTGCTGTTAGTCAGTGAAA 107



164 GCTGACTGAGTCTCCAGTTCAGTGTGACATGGTCAATG 213  
 31 Yala.....LeuLeuProLeuGlnL 38  
 214 ACCTAAGGCTAATAATCCTCATATGGCATGTTGGGTTCAC 263  
 38 euAspPheGlyLeuSerCysLeu..... 45  
 264 TGGATGACCGAAAGCTGGCATTAACATGACGTCAATGGCACAGAAC 313  
 46 .....GluGlu 47  
 314 CCACTTACAGTCACACCAGCATACACACACACACACAC 363  
 47 glu.....PhenLeu 51  
 364 GGAGACTGAGGATCTGCTCACATAGTCACATAGTCACATAGTCAC 413  
 51 algySerLeuLeuLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPhe 67  
 414 TGTCAAGCTTGGAGTGTGGGGATGTGGCTCATCTGGTGGTGG 463  
 68 LeuLeaPheGlySerGlyAlaIleLeuGlySerAsnLeuVa 84  
 464 CTCGGGAAACTGGAGGATCAAGCAATGTCGCTGAAACAGCC 513  
 84 LeuLeuAlaGlySerLeuThrLeuGly.....LeuAlaGlySerI 98  
 514 CTCATGACTGGGCCCTCTGATGGATGTCCTCAAAATTGGACCGGCAC 563  
 98 euAlaTpleuLeuLeuGlyArgAlaValValGlyPheAlaIleSerLeu 114  
 564 ACCCCCTCATCATGGTGGACCAAGTGTTAGACTGTATTGGTGGCTA 613  
 115 SerSerMetAlaCysCysIleIleuSerGluLeuValGlyProArgG 131  
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 664 CAGGGGCGCCCTGGFACTCTTCACCAACTGGCCCTGACAGSCATC 713  
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 163 GlyTrpArgHisMetPheGlyrpAlaThrAlaProAlaValLeuGlnSe 179  
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 179 rLeuSerLeuLeuPheLeuProAlaGly..... 188  
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 861 TGGAAAGGGAAAGTCAGGGCAAAAGACTGAAGAGACTAAAGGAAC 910  
 205 Glu.....AlaProIysLeuG 210  
 911 GAGGATGTCCACAAAGATTAATGAGATGAGAAAGAAAGGAGGGC 960  
 210 yProGlyArgProArgTrpSerPheLeuAspLeuPheArgAlaArgAspA 227  
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 ::::: 1553 TCTTTAAAGTCCAGAACCAAAGGAAAGCTTGTAGGAAATGGCTGC 1602  
 510 nGlnPheGlnIysArg 515  
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 seq\_name: gb\_est1:Al449904  
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 LOCUS Al449904 396 bp mRNA  
 DEFINITION Homo sapiens fetal lung (Stavrides GS) Homo sapiens sequence.  
 ACCESSION Al449904

VERSION	AL449904.1	GI:	111181529
KEYWORDS			
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ORGANISM	Homo sapiens		
REFERENCE	EST.		
AUTHORS	human.		
TITLE			
JOURNAL			
COMMENT			
source			
FEATURES			
ORIGIN			
BASE COUNT			
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Quality:	398.00	Length:	79
Ratio: 5.038	Gaps: 0	Percent Identity: 100.000	
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alignment_block:			
US-09-652-292-2 X AL449904	77 a 122 c 99 g 97 t 1 others		
Align seg 1/1 to: AL449904	from: 1 to: 396		
463 SerLeuSerPheLeuAspLeuIleGlyIleLeuSerIlePhePhrPhrPh	479		
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2 AGCCTCTCTCTGCTCGTGCAGTCATGGGCCATGGCTGTGACCTT	51		
479 IleLeuIleGlyLeuLeuAlaLeuIleGlyLeuGlyPhenIleYleuP	496		
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202 CATCGGTACAGCGCATCGAGATCTCGGGCTCC 238			
seq_name: g_blast1:AL614852			
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LOCUS	AL614852	EST	21-APR-1999
DEFINITION	V95608.y1 Soares_mammary_gland_NbMMG	Mus musculus	cDNA clone
IMAGE	515182 5' similar to TR032289	YXCC PROTEIN.	mRNA
SEQUENCE			
ACCESSION	AI614852		
VERSION	AI614852.1	GI: 4624019	
KEYWORDS			
SOURCE			
ORGANISM	Mus musculus		
Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MGI:503734			
COMMENT			
Journal			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs@med.nih.gov			
This clone is available royalty-free through LBNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.			
MGID:503734			
This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)			
Unpublished (2000)			
Contact: Stavrides GS			
The Sanger Centre			
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK			
Email: humquery@sanger.ac.uk			
Sanger Centre name : scc03094.			
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102 TTGTCCGAAACAAAGGCCACCTGTTGGCAGATAAGACAGCTTC	151		
513 GluLysArgPheThrLeuSerPheGlyLeuGlyGlnSerIleSerThrG	529		
152 CAGANGACAGGTACCCGTGACTTGGCCAGGGAGACTCACTCTGG	201		
529 YlleProtrySerArgIleGluIleSerAlaSer 541			
202 CATCGGTACAGCGCATCGAGATCTCGGGCTCC 238			
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IMAGE	515182 5' similar to TR032289	YXCC PROTEIN.	mRNA
SEQUENCE			
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VERSION	AI614852.1	GI: 4624019	
KEYWORDS			
SOURCE			
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Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MGI:503734			
COMMENT			
Journal			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs@med.nih.gov			
This clone is available royalty-free through LBNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.			
MGID:503734			
This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)			
Unpublished (2000)			
Contact: Stavrides GS			
The Sanger Centre			
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK			
Email: humquery@sanger.ac.uk			
Sanger Centre name : scc03094.			
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IMAGE	515182 5' similar to TR032289	YXCC PROTEIN.	mRNA
SEQUENCE			
ACCESSION	AI614852		
VERSION	AI614852.1	GI: 4624019	
KEYWORDS			
SOURCE			
ORGANISM	Mus musculus		
Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MGI:503734			
COMMENT			
Journal			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs@med.nih.gov			
This clone is available royalty-free through LBNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.			
MGID:503734			
This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)			
Unpublished (2000)			
Contact: Stavrides GS			
The Sanger Centre			
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK			
Email: humquery@sanger.ac.uk			
Sanger Centre name : scc03094.			
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LOCUS	AI614852	EST	21-APR-1999
DEFINITION	V95608.y1 Soares_mammary_gland_NbMMG	Mus musculus	cDNA clone
IMAGE	515182 5' similar to TR032289	YXCC PROTEIN.	mRNA
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ORGANISM	Mus musculus		
Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MGI:503734			
COMMENT			
Journal			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs@med.nih.gov			
This clone is available royalty-free through LBNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.			
MGID:503734			
This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)			
Unpublished (2000)			
Contact: Stavrides GS			
The Sanger Centre			
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK			
Email: humquery@sanger.ac.uk			
Sanger Centre name : scc03094.			
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529 YlleProtrySerArgIleGluIleSerAlaSer 541			
202 CATCGGTACAGCGCATCGAGATCTCGGGCTCC 238			
seq_name: g_blast1:AI614852			
seq_documentation block:			
LOCUS	AI614852	EST	21-APR-1999
DEFINITION	V95608.y1 Soares_mammary_gland_NbMMG	Mus musculus	cDNA clone
IMAGE	515182 5' similar to TR032289	YXCC PROTEIN.	mRNA
SEQUENCE			
ACCESSION	AI614852		
VERSION	AI614852.1	GI: 4624019	
KEYWORDS			
SOURCE			
ORGANISM	Mus musculus		
Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MGI:503734			
COMMENT			
Journal			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs@med.nih.gov			
This clone is available royalty-free through LBNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.			
MGID:503734			
This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)			
Unpublished (2000)			
Contact: Stavrides GS			
The Sanger Centre			
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK			
Email: humquery@sanger.ac.uk			
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2 AGCCTCTCTGCTCGTGCAGTCATGGGCCATGGCTGTGACCTT	51		
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52 CCGCTCTACGGCTGACCCGTGACCGCTGCGCTGGCTTCAGCTATTTAT	101		
496 IleValProGluIleLysGlyGlnSerLeuIleAspGlnGlnPhe	512		
102 TTGTCCGAAACAAAGGCCACCTGTTGGCAGATAAGACAGCTTC	151		
513 GluLysArgPheThrLeuSerPheGlyLeuGlyGlnSerIleSerThrG	529		
152 CAGANGACAGGTACCCGTGACTTGGCCAGGGAGACTCACTCTGG	201		
529 YlleProtrySerArgIleGluIleSerAlaSer 541			
202 CATCGGTACAGCGCATCGAGATCTCGGGCTCC 238			
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seq_documentation block:			
LOCUS	AI614852	EST	21-APR-1999
DEFINITION	V95608.y1 Soares_mammary_gland_NbMMG	Mus musculus	cDNA clone
IMAGE	515182 5' similar to TR032289	YXCC PROTEIN.	mRNA
SEQUENCE			
ACCESSION	AI614852		
VERSION	AI614852.1	GI: 4624019	
KEYWORDS			
SOURCE			
ORGANISM	Mus musculus		
Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MGI:503734			
COMMENT			
Journal			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs@med.nih.gov			
This clone is available royalty-free through LBNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.			
MGID:503734			
This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)			
Unpublished (2000)			
Contact: Stavrides GS			
The Sanger Centre			
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK			
Email: humquery@sanger.ac.uk			
Sanger Centre name : scc03094.			
Location/Qualifiers			
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Align seg 1/1 to: AL449904	from: 1 to: 396		
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1     1     1     1     1     1     1     1     1			
2 AGCCTCTCTGCTCGTGCAGTCATGGGCCATGGCTGTGACCTT	51		
479 IleLeuIleGlyLeuLeuAlaLeuIleGlyLeuGlyPhenIleYleuP	496		
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496 IleValProGluIleLysGlyGlnSerLeuIleAspGlnGlnPhe	512		
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